



10077137 Sequence Listing
SEQUENCE LISTING

<110> MACKAY, FABIENNE
BROWNING, JEFFREY
AMBROSE, CHRISTINE
TSCHOPP, JURG
SCHNEIDER, PASCAL
THOMPSON, JEFFREY

<120> BAFF RECEPTOR (BCMA), AN IMMUNOREGULATORY AGENT

<130> 08201.0027

<140> 10/077,137

<141> 2002-02-15

<150> PCT/US00/22507

<151> 2000-08-16

<150> 60/149,378

<151> 1999-08-17

<150> 60/181,684

<151> 2000-02-11

<150> 60/183,536

<151> 2000-02-18

<160> 9

<170> PatentIn Ver. 3.3

<210> 1

<211> 184

<212> PRT

<213> Homo sapiens

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Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
50 55 60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65 70 75 80

Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
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130	135	140	
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Thr 165	Asn 170	Asp 175	Tyr 180
Ile 185	Glu 190	Lys 195	Val 200
Thr 205	Thr 210	Lys 215	

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 gtaatgcaag tgtgaccaat tcagtgaag gaacgaatgc gattctctgg acctgtttgg 180
 gactgagctt aataatttct ttggcagttt tcgtgctaag gtttttgcta aggaagataa 240
 gctctgaacc attaaaggac gagtttaaaa acacaggatc aggtctcctg ggcatggcta 300
 acattgacct ggaaaagagc aggactgggtg atgaaattat tctccgagag gcctcgagta 360
 cacgggtggaa gaatgcacct gtgaagactg catcaagagc aaaccgaagg tcgactctga 420
 ccattgcttt ccactcccag ctatggagga aggcgcaacc attctgtcac cacgaaaacg 480
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 tctgctaggt aa 552

<210> 3
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 Thr 70 Gly 75 Met 80 Leu 85 Gln 90 Met 95 Ala 100 Gly 105 Gln 110 Cys 115 Ser 120 Gln 125 Asn 130 Glu 135 Tyr 140 Phe 145
 Asp 150 Ser 155 Leu 160 Asp 165 Val 170 Thr 175 Met 180 Leu 185 Gln 190 Met 195 Ala 200 Gly 205 Gln 210 Cys 215 Ser 220 Gln 225
 Asn 230 Glu 235 Tyr 240 Phe 245 Asp 250 Ser 255 Leu 260 His 265 Ala 270 Cys 275 Ile 280 Pro 285 Cys 290 Gln 295 Leu 300
 Arg 305 Cys 310 Ser 315 Ser 320 Asn 325 Thr 330 Pro 335 Pro 340 Leu 345 Thr 350 Cys 355 Leu 360 His 365 Ala 370 Cys 375 Ile 380
 Pro 385 Cys 390 Gln 395 Leu 400 Arg 405 Cys 410 Ser 415 Ser 420 Asn 425 Thr 430 Pro 435 Pro 440 Leu 445 Thr 450 Cys 455 Gln 460
 Arg 465 Tyr 470 Cys 475 Asn 480 Ala 485 Ser 490 Val 495 Thr 500 Asn 505 Ser 510 Val 515 Lys 520 Gly 525 Gln 530 Arg 535 Tyr 540
 Cys 545 Asn 550 Ala 555 Ser 560 Val 565 Thr 570 Asn 575 Ser 580 Val 585 Lys 590 Gly 595 Val 600 Asp 605 Lys 610 Thr 615 His 620
 Thr 625 Cys 630 Pro 635 Pro 640 Cys 645 Pro 650 Ala 655 Pro 660 Glu 665 Leu 670 Leu 675 Gly 680 Gly 685 Pro 690 Ser 695 Val 700

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
165 170 175
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
180 185 190
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val
195 200 205

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ttgcatgctt gcataacctg tcaacttcga tgttcttcta atactcctcc tctaacatgt 180
cagcggttatt gtaatgcaag tgtgaccaat tcagtgaag gagtcgacaa aactcacaca 240
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aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 360
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20 25 30
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
35 40 45
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
50 55 60
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
65 70 75 80
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
85 90 95
Gly Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
100 105 110
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
115 120 125
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 6
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acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 180
cagccggaga acaactacaa gaccacgcct cccgtgttgg actccgacgg ctcttcttc 240
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 300
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<210> 7
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<400> 7
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
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Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
          20          25          30
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
          35          40          45
Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
          50          55          60
Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
          65          70          75          80
Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
          85          90          95
Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
          100          105          110
Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
          115          120          125
Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
          130          135          140
Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
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Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
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Ile Glu Lys Ser Ile Ser Ala Arg
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<210> 8
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agctgctctt gctgcatttg ctctggaatt ctgttagaga tattacttgt ccttccaggc 180
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<210> 9
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          20          25          30
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
          35          40          45
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
          50          55          60
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
          65          70          75          80
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
          85          90          95
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
          100          105          110
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
          115          120          125
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
          130          135          140
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
          145          150          155          160
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
          165          170          175
Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
          180          185          190

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Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met
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	210					215					220				
Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu
225					230					235					240
Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly
				245					250					255	
Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu
			260					265					270		
Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala	Leu	Lys	Leu	Leu			
		275					280					285			